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GenCore version 5.1.3
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OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	December 15, 2002, 00:18:43 ; Search time 3175 Seconds (without alignments) 1668.255 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-762-105-14 182 1 gagctcgctccccgccgtctgactggtggacaggctagc 182
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 seqs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq Maximum DB seq .	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:* 1: gb_ba:* 2: gb_htg:* 3: gb_in:* 4: gb_on:* 5: gb_ov:* 6: gb_pat:* 8: gb_pi:* 9: gb_pi:* 10: gb_sr:* 11: gb_sr:*

is the number of results predicted by chance to have a Pred. No.

em_htgo_other:*

em_htgo_hum:* em_htgo_mus:*

em_htg_mam:* em_htg_vrt:*

SYN 24-APR-2000

F176637 5270 bp DNA linear SYN 24-APF lastid transformation vector pMSK49 plastid targeting region.

AF176637 AF176637.1 GI:7637848

ORGANISM REFERENCE AUTHORS

JOURNAL

TITLE

KEYWORDS SOURCE

AF176637

RESULT 1
AF176637/C
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DEFINITION
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VERSION

em_htg_other:*

em_htg_inv:* em_htg_mus:* em_htg_pln:* em_htg_rod:*

em_vi:* em_htg_hum:*

em_un:*

em_pl:* em_ro:* em_sts:*

em_fun:* em_hum:* gb_vi:* em_ba:*

em_om:* em_or:* em_in:* еш_ши:*

еш_о∨:* em_pat:

*: un_db

ALIGNMENTS

Plastid transformation vector pMSK49.
Plastid transformation vector pMSK49
artificial sequences; vectors.

1 (bases 1 to 5270)
Khan,M.S. and Maliga,P.
Khan,M.S. and mibiotic resistance marker for tracking plastid transformation in higher plants
Nat. Biotechnol. 17 (9), 910-915 (1999)

AF176637 Plastid t
AX076661 Sequence
AX13714 Sequence
E51179 Method for
701453 Tobacco (N.
700155 Tobacco (N.
700165 Tobacco (N.
700165 Tobacco (N.
718934 Solanum nig
200044 Nicotiana t
AJ316582 Atropa be
AR1316582 Atropa be
AR171710 Sequence
AR17711 Sequence
U12809 Transformat
U12819 Transformat
U12815 Transformat
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U12818 Transformat
U12819 Transformat
AF061065 Plastid
U12819 Transformat
U12819 Transformat
AF061065 Plastid
U12819 Transformat
AF061065 Plastid
U12813 Transformat
AF312391 Chloropla
AF312392 Chloropla
AF312392 Chloring vec
X54208 Cloning vec AX191649 Sequence V01146 Genome of b AR004778 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES PET31F1P CVPRSET5C CVPRSET6C CVPRSET6B CVPRSET6B CVPRSET6A CVPRSET6A CVPRSET6A CVT7NDE CVPGEMEX1 CVPGEMEX2 XXU12815 XXU12813 XXU12813 AY005806 CTR312391 CTR312393 AF176637 AX076661 AX137514 E51179 E51197 TOBCPTGVR CHNPTRNVI CCRY18934 CCRYXX CHNTXX CHNTXX ABE316582 ABE316582 ABE316582 ABE316582 ARI71710 ARI717110 ARI71710 AR AF061065 XXU12814 T7CG AR004778 AX191649 <u>B</u> 47.1 47.1 47.1 47.1 766 47.1 71.1 72.1 72.1 72.1 72.1 73.2 74.2 7 Length Query

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PAT 30-MAY-2001
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            complement(3683. .3858)
//note="printly3f0+Db/Rec promoter and translation control region contained in SacI-NheI fragment."
3859. .3879
//note="sacI, EcoRI and PstI restriction sites"
1330 c 1145 g 1417 t
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61.1%; Score 111.2; DB 6; Length 168;
Best Local Similarity 88.7%; Pred. No. 5.1e-25;
Matches 133; Conservative 0; Mismatches 13; Indels 4
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Best Local Similarity 100.0%; Score 182; DB 12;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 182; Conservative 0; Mismatches 0;
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unidentified
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1 (bases 1 to 168)
Staub,J.M.
Enhanced expression of proteins using gfp
Patent: WO 010431-A 1 18-JAN-2001;
Calgene LLC (US)
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/organism="unidentified"
/db_xref="taxon:32644" 41
a 31 c 51 g 41
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Sequence 16 from Patent EP1076095.
AX137514
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AX07661 1 GI:12711193
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gene="aadAl1gfp-S3"
complement(3699..3712)
complement(3699..3312)
complement(3699..3600)
complement(3699..3600)
complement(3699..3600)
complement(3699..3600)
complement(3699..3600)

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E 99403345

D 10471936

CE 2 (bases 1 to 5270)

NRS Khan,M.S. and Maliga.P.

E Direct Submission

NAL Submitted (09-AuG-1999) Waksman Institute, Rutgers -

Frelinhuysen Road, Piscataway, NJ 08854, USA

Frelinhuysen Road, Piscataway, NJ 08854, USA

1. 5270

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source / Ab_xref - taxon:120083"

/ focus

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complement(<1. 1332)
/product="165 ribosomal RNA"
complement(1564. 1635)
/product="RRN-Val"
1885. 1910
/noce="Clal and HindIII restriction sites"
/gene="Clab and HindIII restriction sites"
/gene="psbA"
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/organism="Nicotiana tabacum"
/organelle="plastid"
/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/organelle="plastid"
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misc_feature
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PAT 31-JAN-2002
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Nicotiana tabacum.
Nicotiana tabacum.
Nicotiana tabacum.
Nicotiana tabacum.
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

| (bases 1 to 127) | Nakashita, Wamaguchi, I., Yoshioka, K. and Doi, Y. Process for producing polyester Patent: JP 2001046074-A 16 20-FEB-2001; RIKAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 766)
Tohdoh, N., Shinozaki, K. and Sugiura, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PI HIDEO NAKASHITA,ISAMU YAMAGUCHI,KEIKO YOSHIOKA,YOSHIHARU DOI PC C12N15/09,A0145/00,C12N5/10,C12N9/10,C12P7/62, PC C12N15/00,C12N5/00
CC CC CC Location/Qualifiers
FT source L. 127
/organism='Nicotiana tabacum (tobacco)'.
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16S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val.
Tobacco (N.tabacum, var. bright yellow 4) chloroplast DNA, clone
                       11 TIGCTCCCCCCCCCTCCTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGG 70
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Tobacco (N.tabacum) Val-tRNA gene and 16S rRNA gene 5' end.
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Pred. No. 7.8e-17;
0; Mismatches 2;
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/organism="Nicotiana tabacum"
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JP 2001046074-A/16
20-FEB-2001
                                                                                                                                                                                                                                                                          Process for producing polyester.
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97.8%;
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JP 2001046073-A/16.
Nicotiana tabacum.
Nicotiana tabacum.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Hagnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.

1 (bases I to 127)
Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
Method for transforming plant and transformed plant
Patent: JP 2001046073-A 16 20-FEB-2001;
RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
                                            common tobacco.

Nicoliana tabacum

Nicoliana tabacum

Nicoliana tabacum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

(bases 1 to 127)

Yamaguchi,I., Nakashita,H., Yoshioka,K. and Doi,Y.

Processes for transformation of plants, transformed plants and
Patent: Ep 1076095-A 16 14-FEB-2001;
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PN JP 2001046673-A/16
PD 20-FEB-2001
PF 99-AUG-1999 JP 1999225832
PR 1 HIDBO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI PC 121015/09, A0115/00, C12N5/10, C12N9/10, C12P7/62, PC C12N15/00, C12N5/00, C12N5/10, C12N9/10, C12P7/62, PC C12N15/00, C12N5/10, C12N9/10, C12P7/62, PC C12N15/00, C12N5/10, C12N
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'organism='Nicotiana tabacum-(tobacco)'
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Pred. No. 7.8e-17;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 127;
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E51179
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Pred. No. 7.8e-17;
0; Mismatches 2; Indels
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AX137514.1 GI:14273708
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1 Similarity 97.8%;
87; Conservative 0
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97.88;
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Best Local Similarity
Matches 87; Conserv
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Gaps

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Direct Submission

Direct Submission

C. Submitted (16 FEB-1993) G.V. Horvath, Biolgoical Research Centre, Institute of Plant Phys., Hungarian Academy of Science, PO BOX 521, Institute of Plant Phys., Hungarian Academy of Science, PO BOX 521, Institute of Plant Phys., Hungarian Academy of Science, PO BOX 521, Institute of Plant Files

For a 1. 3274

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHNPTRNVI S274 bp DNA Linear PLN 04-JUN-1993 N.plumbaginifolia chloroplast 16SrDNA, trnV and trnI genes for 16S ribosomal RNA, transfer RNA-Val and transfer RNA-Ile (5'exon).
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                                                                                                                                                                                                                                                                       5 TCGCTCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGG
                                                            Length 2113;
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/anticodon=(pos:972. .974,aa:Val)
1226. .2714
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                                                  Score 85.8; DB 8;
pred. No. 1e-16;
0; Mismatches 2;
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/gene="16SrDNA"
1226. 2714
1226. 2714
/gene="16SrDNA"
/product="16S ribosomal RNA"
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/gene="trnv"
/product="tRNA-Val"
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/gene="trn1"
/product="tRNA-Ile"
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Horvath, G.V.
                                                            Query Match
Best Local Similarity 97.8%;
Matches 87; Conservative
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V00165 J01453 1799
V00165.1 GI:11799
15S ribosomal RNA; ribosomal RNA; transfer RNA; transfer RNA-Val.
Common tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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Eukaryota; Micotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots;
Aspermacophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterida; I; Solanales; Solanaceae; Nicotiana.

1 (bases 628 to 2113)
1 (bases 628 to 2113)
1 (bases 628 to 2113)
1 (bases 628 to 213)
1 (bases 628 to 2
                                                                                                                                                                                                                                                        transcription initiation, based on an in vitro assay with E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 766)
Tohdoh, N., Shinozaki, K. and Sugiura, M.
Sequence of a putative promoter region for the rRNA genes of
tobacco chloroplast DNA
Nucleic Acids Res. 9 (20), 5399-5406 (1981)
82059514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="codon recognized; GUC; Val-tRNA (NAR: 2063)"
628. >766
Product="16S ribosomal RNA"
1 145 c 215 g 206 t
Sequence of a putative promoter region for the rRNA genes of tobacco chloroplast DNA Nucleic Acids Res. 9 (20), 5399-5406 (1981) 82059514 7029469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85.8; DB 8; Length 766; Pred. No. 9.3e-17; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iocation/Qualifiers
1. .2113. "Nicotiana tabacum"
/organism="Nicotiana tabacum"
/organism="piastid:chloroplast"
/db_xref="taxon:4097"
328. .399
/product="TRNA-Val"
628. .2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/product="16s ribosomal RNA"
473 c 649 g 461 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.8%;
Matches 87; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA polymerase.
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VERSION
KEYWORDS
SOURCE
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Length 3274;

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Nicotiana tabacum chloroplast genome DNA.

200044 S54304
200044.1 GI:292423.0
200044.1 GI:292424.0
200044.1 GI:29242.0
200044.2 GI:29242.0
200044.1 GI:29242.0
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WLLAASRKRPGRNMAFKLSSELVDAAKGSGDAIRKKEETHRWAEANRAFAHFR"
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Pred. No. 1.2e-16;
0; Mismatches 2;
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                                                         /transl_table=11
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                                                                                                                                                                                                                                                                                           /number=1
5730, .6265
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6345. 6812
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97.88;
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Solanum nigrum chloroplast tRNA-Ala, tRNA-1le, 165 rRNA, tRNA-Val,
rps1, rps7, ndhB genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16S ribosomal RNA, 16S rRNA gene; NADH dehydrogenase subunit; ndhB gene; ribosomal protein S12; ribosomal protein S7; rps12 gene; rps7 gene; transfer RNA-Ala; transfer RNA-Ile; transfer RNA-Val; tRNA-Ala gene; tRNA-Ile gene; tRNA-Val gene.
Dlack nightshade.
Plastid Solanum nigrum
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Kavanagh, T. A., Thanh, N. D., Lao, N. T., McGrath, N., Peter, S. O., Horvath, E. M., Dix, P. J. and Medgyesy, P. Horvath, E. M., Dix, P. J. and Medgyesy, P. Homeologous plastid DNA transformation in tobacco is mediated by multiple recombination events
                                                                                                          Direct Submission
Submitted (19-APR-1999) T.A. Kavanagh, University of Dublin,
Department of Genetics, Trinity College, Dublin 2, IRELAND
Location/Qualifiers
                                                                                 TCGCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGG
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Pred. No. 1.1e-16;
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join(<5498, .5729,6266, .6291)
/gene="rps12"
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/gene="16S rRNA"
/product="16S ribosomal RNA"
3797. .3869
/gene="tRNA-Val"
3797. .3660
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John Trysl2"

John Trysl2"
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/organism-"Solanum nigrum"
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join(5498. .5729,5730.
/gene="rps12"
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/db_xref="taxon:4112"
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Jim is designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of ribulose 1.5-bisphosphate carboxylase is designated as A strand and the complementary strand as B strand.

Nucleotide sequence of the B strand is presented large single copy region (LSC): 1.2027 (25341 bp) Small single copy region (SSC): 112027 (25341 bp) Small single copy region (SSC): 112028 (1871 bp) Inverted repeat A (IRA) region (SSC): 125938 (1871 bp) An alphabetical index of tobacco chloroplast genes and ORFs GENE NUCLEOTIDE NUMBER (FROM) acc)
Submitted (27-FEB-1998) T. Tsudzuki, Data Processing Center, Aichi-Gakuin University, 12 Araike, Iwasaki, Nisshin, Aichi 0. Aichi 0. Defore Jan 17, 2002 this sequence version replaced gi:264799, 21.11807. The circular tobacco chloroplast DNA sequence is presented in a finearized form by cutting at the junction (JLA) between IRA and
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SM Plastid Nicotiana tabacum streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Nicotiana.

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

Shinozaki, K., Ohme, W., Tanaka, M., Wakasugi, T., Hayashida, N., Matsubayashi, T., Zaita, N., Chunwongse, J., Oberganaghi, Shinozaki, K., Ohto, C., Torazawa, K., Meng, B.Y., Sugita, M., Deno, H., Kamogashira, T., Yamada, K., Kusuda, J., Takaiwa, F., Kato, A., Tohdoh, N., Shinada, H. and Sugiura, M.

Tohdoh, N., Shinada, H. and Sugiura, M.
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A phylogenetic analysis of monocotyledons based on the chloroplast
agene rps4, using parsimony and a new numerical phenetics method
MOI: Phylogenet. Evol. 4 (3), 257-282 (1995)
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Runnimalaiyaan, M. and Nielsen, B.L.
Runnimalaiyaan, M. and Nielsen, B.L.
Ripe mapping of replication origins (ori A and ori B) in Nicotiana tabacum chloroplast DNA
Nucleic Acids Res. 25 (18), 3681-3686 (1997)
                        M-protein; PSII N-protein; replication origin; ribosomal protein L14; ribosomal protein L16; ribosomal protein L15; ribosomal protein L12; ribosomal protein L21; ribosomal protein L23; ribosomal protein L23; ribosomal protein L23; ribosomal protein L32; ribosomal protein L31; ribosomal protein L32; ribosomal protein L31; ribosomal protein S11; ribosomal protein S12; ribosomal protein S15; ribosomal protein S15; ribosomal protein S15; ribosomal protein S15; ribosomal protein S19; ribosomal protein S2; ribosomal protein S3; ribosomal protein S3; ribosomal protein S3; ribosomal protein S4; ribosomal protein S4; ribosomal protein S6; ribosomal protein S8; ribolsomal S8;
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Ayliffe, M.A. and Timmis, J.N.
Plastid DNA sequence homologies in the tobacco nuclear genome Mol. Gen. Genet. 236 (1), 105-112 (1992)
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Morton, B.R. and Clegg, M.T.

Mortophast DNA mutational hotspot and gene conversion noncoding region near rbcL in the grass family (Poaceae)

Curr. Genet. 24 (4), 357-365 (1993)
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Processing of histidine transfer RNA precursors
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Nucleic Acids Res. 19 (11), 3150 (1991)
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Submitted (12-AUG-1986)
9 (bases 1 to 155939)
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Plastid Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 155844)
Shinozaki, K., Ohme, M., Tanaka, M., Wakasugi, T., Hayashida, N., Matsubayashi, T., Zaita, N., Chunwongse, J., Obokata, J.,
Yamaguchi-Shinozaki, K., Ohto, C., Torazawa, K., Meng, B.Y., Sugita, M., Tohdoh, N., Shimada, H. and Sugiura, M., Takaiwa, F., Kato, A.,
Tohdoh, N., Shimada, H. and Sugiura, M.
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Nadot,S., Bittar,G., Carter,L., Lacroix,R. and Lejeune,B.
A phylogenetic analysis of monocotyledons based on the chloroplast gene rps4, using parsimony and a new numerical phenetics method Mol. Phylogenet. Evol. 4 (3), 257-282 (1995)
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Kunnimalalyaan, M. and Nielsen, B.L.
Fine mapping of replication origins (ori A and ori B) in Nicotiana
tabacum chloroplast DNA
Nucleic Acids Res. 25 (18), 3681-3686 (1997)
1.23; ribosomal protein 1.32; ribosomal protein 1.33; ribosomal protein 1.36; ribosomal protein 1.31; ribosomal protein 1.31; ribosomal protein 1.31; ribosomal protein 1.31; ribosomal protein 1.35; ribosomal 1.35; ribosoma
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Ayliffe, M.A. and Timmis, J.N.
Plastid DNA sequence homologies in the tobacco nuclear genome Mol. Genet. 236 (1), 105-112 (1992)
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Morton,B.R. and Clegg,M.T.
A chloroplast DNA mutational hotspot and gene conversion in noncoding region near rbcL in the grass family (Poaceae) Curr. Genet. 24 (4), 357-365 (1993)
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Submitted (27.FEB-1998) T. Tsudzuki, Data Processing Center,
Alchi-Gakuin University, 12 Araike, Iwasaki, Nisshin, Aichi
470-0195, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitchelson, K. and Stephen, J. Processing of histidine transfer RNA precursors in tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fine structural features of the chloroplas
the sequenced chloroplast genomes
Wucleic Acids Res. 19 (5), 983-995 (1991)
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9 (bases 1 to 155939)
Tsudsuki,T.
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OGNNERNY OF or TableCore Jan 17, 2002 this sequence version replaced gil264799, gil.1867 and gil.1867 counts to before Jan 17, 2002 this sequence with and linearized form by cutting at the junction (JJA) between 184 and Linearized form by cutting at the junction (JJA) between 184 and Linearized form by cutting at the junction (JJA) between 184 and Linearized form by cutting at the junction (JJA) between 185 and Linearized form by cutting at the junction (JJA) between 186 and the complementary at and as B strand. In presented the complementary at and as B strand. In presented the presented to the property of the junction (JJA) between 186 and the complementary at and as B strand. In presented the presented to th
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GI:20068310
6S ribosomal RNA; 4.5s ribosomal RNA; 5.
Tibosomal RNA; 23s ribosomal RNA; 4.5s ribosomal RNA; 5.
Tibosomal RNA; accD gene; acetyl-CoA carboxylase beta subunit;
ATP-dependent protease; atpA gene; ATP-ase subunit; NADH dehydrogenase NDS subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND4 subunit; 
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0; Mismatches 2; Indels 0;
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PNSALRKVARVRLTSGFEITAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGTL
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VTSSLIRETTENESANEGYRFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLA
AWPVVGIWFTALGISTWAFNLNGFNFNQSVVDSQGRVINTWADIINRANLGMEVWHER
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LEILVQTLRYWVKDASSLHLLRFFLHEYWNLNSLITSKKPGYSFSKKNKRFFFFLYNS
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FMHYVRYQGKSILASKGTFLLINKWKFYLVNFWQCHFSLCFHTGRIHINQLSNHSRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                     join(complement(100895. .101126),
complement(100360. .100894), complement(100333. .100359),
complement(72478. .72591), 142431. .142662, 143198. .143223)
/gene="rps12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSVFIIAFIAAPPUDIDGIREPVSGSLLYGNNIISGAIIPTSAAIGLHFYPIWEAASV
DEWLYNGGPYELIVLHFLLGVACYMGREWELSFRLGMRPWIAVAYSAPVAAATAVFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(1769. .1804,1805. .4323,4324. .4360))
/gene="tRNA-Lys (UUU)"
complement(join(1769. .1804,4324. .4360))
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72479. .72591))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(complement(72478. .72591),142431, .142662,143198. .14323)
                                                                                                                                                                                                                                                   /product="ribosomal protein S12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PSII 32 kD protein"
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/db_xref="GI;20068311"
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              l. .156687
∕organism="Atropa belladonna"
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complement(2068. 3597)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(494. .1555)
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complement(494. .1555)
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                                                                                                                                                                                                                                                                                                                                                                                                                              DAVGVKDRQQGRSKYGVKKPK
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Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches
Institut, Ludwig Maximilians Universitaet Muenchen, Menzinger Str.
67, Muenchen, Bavaria B6058, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The nucleotide sequence of the plastid chromosome of Atropa belladonna (deadly nightshade) and its comparison with that of Nicotiana tabacum with emphasis on sequence elements relevant for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trna-Pro(UGG) gene; trna-Ser (GGA) gene; trna-Ser(GCU) gene; trna-Ser(UGA) gene; trna-Thr(UGU) gene; trna-Thr(UGU) gene; trna-Thr(UGU) gene; trna-Trp(CCA) gene; trna-Try(CCA) gene; trna-Try(CGA) gene; trna-Val (GAC) gene; trna-Val (UAC) gene; yc4 protein; yCFI gene; Ycf1 protein; ycf1 gene; ycf1 gene; Ycf1 gene; Ycf3 protein; ycf3 gene; Ycf9 protein; ycf4 gene; Ycf9 gene; Ycf9 protein.
dehydrogenase ND5 subunit; ndhA gene; ndhB gene; ndhC gene; ndhD
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Herrmann,R.G. and Maier,R.
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Schmitz-Linneweber, C.
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ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

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Applicable DNA circular PLN 05-APR-2002

Apriles Delladonna Complete Plastid Chromosome, strain Ab5p(kan).

Applicable Delladonna Complete Plastid Chromosome, strain Ab5p(kan).

Applicable I CI:20068310

Applicable Complete Dlastid Chromosomal RNA; 55

166 ribosomal RNA; 235 ribosomal RNA; 4.55 ribosomal RNA; 55

167 ribosomal RNA; acc0 gene; acetyl-CoA carboxylase beta subunit;

Arp-dependent protease; atpA gene; ArPase alpha subunit; ArPase

beta subunit; TI; Arpase epsilon subunit; ArPase subunit; ArPase subunit; II; Arpase

subunit III; Arpase subunit IV; atpB gene; atpF gene; atpP gene; atpH gene; atpI gene; catalytic subunit; ccsA gene; ccmA gene; cppF gene; cyt b6/f complex subunit IV; cyt b6/f complex subunit IV; cyt b6/f complex subunit; NADH delydrogenase ND6 subunit; NADH dehydrogenase ND6 subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND2 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND3 subunit; NADH dehydrogenase ND5 subunit; NADH dehydrogenase ND6 subunit; NADH dehydrogenase ND6 subunit; NADH dehydrogenase ND6 subunit; NADH dehydrogenase ND6 subonit; NADH dehydrogenase ND6 subonit; NADH dehydrogenase ND6 subonit; NADH dehydrogenase ND6 subonit; NADH dehy
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/umber=2
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MGYLSSVRLNPSMYRSQMLENSFIINNAIKKFDTLVPIIPLIGSLAKENFCTVLGHPI
SKPYWSDLSDSDIIDRFGRICRNLFHYYSGSSKKKTLYRIKYILRLSCARTLARKHKS
TYRTFLKRSGSELLEEFLTSEEQVLSLTFPRASSSLWGVYRSRIWYLDIFCINDLANY
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DD 102861 TTGCTCCCCGCCGTCGTTCAATGAGATGGATAAGAGCTCGTGGGATTGACGTGAGGG 102920
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                                                                                                                                                                                                                                                                                                                                                               complement(5050. .6138)
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complement(join(5050. .5276,6099. .6138))
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/note="codon recognized: AAA"
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gene; petL gene; petH gene; potential heme-binding protein; PS1 gene; pasL ge
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Herrmann, R.G. and Maier, R.M.
Herrmann, R.G. and Maier, R.M.
The nucleotide sequence of the plastid chromosome of Atropa
belladonna (deadly nightshade) and its comparison with that of
Nicotiana tabacum with emphasis on sequence elements relevant for
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Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches
Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches
Institut, Ludwig Maximilians Universitaet Muenchen, Menzinger Str.
67, Muenchen, Bavaria 80638, Germany
Location/Qualifiers
1. 156887
/organism-"Atropa belladonna"
/strain-"Ab5p(kan)"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
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Schmitz-Linneweber, C.
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/trānslation="MVKLRLKRCGRKQRAVYRIVAIDVRSRREGKDLRKVGFYDPIKN
QTYLNVPAILYFLEKGAQPTGTVQDILKKAEVFKELRPNQPKFN"
complement(5050. .5276)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 184)
Bogosian, G., O'Neil, J.P. and Staub, J.M.
Bacterial expression systems based on plastic or mitochondrial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TCGCTCCCCCCCCCCTCCATGAGAATGGATAAGAGCCTCCTGGGGATTGACGTGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 156687;
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                                                                                                                                                                               /gene="rpsi6"
complement(join(5050. .5276,6099. .6138))
/gene="rpsi6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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Pred. No. 1.6e-16;
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Pred. No. 1.1e-16;
0; Mismatches 1;
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                                                                               /note="codon recognized: AAA"
complement(4324. .4360)
/gene="tRNA-Lys (UUU)"
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Patent: US 6218145-A 3 17-APR-2001;
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Sequence 3 from patent US 6218145.
AR145914
AR145914.1 GI:15109103
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/product="tRNA-Lys"
/note="codor
                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5098. .5277)
/gene="rps16"
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complement(7360. .7431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6099. .6138)
                                                                                                                                                              complement(5050, .6138)
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33 c 59 g
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complement(4324.
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ilarity 98.9%;
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Best Local Similarity
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/db.xref="G1:2006879"
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DANGYKRDROGRSKYGVKFRK"
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YPIQGSESDOMPLGISGTRYMIYPROABHNIIMPFRHIGYAGVGGSLFSAMHGSL
YYSSLIRETTENESANMGYREGOEETY WIY VAAHGYFGKLIFOYASFNNSKSLHFFLA
AWPVVGIWFTALGISTWAFNLNGFNFNQSVVDSQGRVINTWANIINRANLGMEWHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMHYVRYQGKSILASKGTFLLINKWKFYLVNFWQCHFSLCFHTGRIHINQLSNHSRDF
WGYLSSVRAHBSWYRSQMLENSFIINMAIKKFDTVBIPLFLGSLARRBNFCTVLGHPI
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TVRTFLKRSGSELLEBFLTSEEQVLSLTFPRASSSLWOYRSRIWTLDIFCINDLANY
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IVEIPFSLRLISSLSSFEGKKILKSHNLRSIHSTFPFLEDNFSHLNYVLDILIPYPVH
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complement(72478. .72591),142431. .142662,143198. .143223)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4323,4324. .4360))
                 complement(join(100334. .100359,100895. .101126,72478. .72591))
                                                                                                                                                                                                                                                                             join(complement(72478. .72591),142431. .142662,
143198. .143223)
/gene="rps12"
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/gene="tRNA-Lys (UUU)"
complement(join(1769. .1804,4324. .4360))
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/product="rodon recognized: CAC"
complement(494. .1555)
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/gene="psbA"
/gene="psbA"
/gene="psbA"
/gene="psbA"
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complement(2068. .3597)
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Unclassified.
Unclassified.
I (bases 1 to 300)
Maliga,P., Carrer,H. and Chaudhuri,S.
Editing-based selectable plastid marker genes
L patent: US 6297054-A 4 02-0CT-2001;
Location/Qualifiers
I. 300
Arganism="unknown" 61 t
                                                                                                           DNA
                                                                                                          AR171710 300 bp
Sequence 4 from patent US 6297054.
AR171710 AR17710.1 GI:17910660
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Unknown.
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AR171710
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Search completed: December 15, 2002, 01:28:14 Job time : 3319 secs

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Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Prrhlacil Spms pro Nucleotide sequenc Nucleotide sequenc Segulatory region 5, and 3, regulato

5, and 3, regulato Prrn promoter sequ Prrn/rbcL/Rubisco Tobacco plastid RR

Regulatory region Plastid 16S rRNA p DNA of upstream re

Chloroplast gene t

Regulatory region Plastid targeting Selectable marker Nucleotide sequenc

Regulatory region Regulatory region Plastid targeting

AAX21433

AAX21408

AAZ61376

targetting region

ALIGNMENTS

98US-0095163. 98US-0095167. 98US-0112257.

03-AUG-1998; 03-AUG-1998; 15-DEC-1998;

99WO-US17806

03-AUG-1999; 17-FEB-2000

Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc Prrn/G10L fusion n Nucleotide sequenc

AAZ61373 AAZ61384 AAZ61374 AAZ61375 AAZ61375 AAZ61375 AAF57902 AAF57902

182 1961 1961 182 161 168 168 168

100.0 100.0 100.0 90.3 87.6 61.1 61.1

126459786

Result Š. 164.4 159.4 1111.2 1111.2 1111.2

Prrn/G10L promoter Nucleotide sequenc

WO200007431-A1

Nucleotide sequenc Nucleotide sequenc Plastid rRNA opero Plastid rRNA opero

Nucleotide sequenc Nucleotide sequenc DNA fragment desig Nucleotide sequenc Nucleotide sequenc

Run on:

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Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of chimeric promoter PrrnLT7g10+DB/Ec.
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7.89
7.89
7.409- a
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141.14
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AAZ61372
AAZ61368
AAF81256
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AAZ61364
AAZ61366
AAZ61365
AAZ61365
AAZ61365
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AAZ61381
AAQ94853
AAZ61371
AAZ61370
AAX21424
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AAX21424
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AAX21409
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AAZ61382
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  AAZ61373 standard; DNA; 182
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 1183
                                        19-JUN-2000
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93.0
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92.2
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90.0
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                                                                                (without alignments)
1335.061 Million cell updates/sec
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3: /SIDSZ/gcgdata/geneseqy-embl/NA1981.DAT:*
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27: /SIDSZ/gcgdata/geneseqy-embl/NA1999.DAT:*
27: /SIDSZ/gcgdata/geneseqy-embl/NA1999.DAT:*
                                                                                                                               1 gagetegeteeceegeegte......tgaetggtggacaggetage 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                    December 15, 2002, 00:17:53; Search time 307 Seconds
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                     Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                 2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                 - nucleic search, using sw model
                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match
                                                                                                                      182
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Perfect score:
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Database

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GC 182
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                                                                                                                                                                  The present sequence represents a chimeric plastid rRNA operon omega-type (Prrn) promoter with the T7 phage gene and plastid comega-type (Prrn) promoter with the T7 phage gene and plastid downstream box. The chimeric promoter is used, as a 5' regulatory sequence, to produce recombinant DNA constructs for expressing sequence, to produce recombinant DNA constructs for expressing the plants. The DNA constructs comprise a 5' regulatory region which includes a promoter of element, a leader sequence and adownstream box element operably linked element, a leader sequence and adownstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory to a coding region of the heterologous protein. The chimeric regulatory to a coding region of the hard efficiency of an mRNA molecule encoded by the DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein agronomic, industrial or pharmaceutical importance, including production agronomic, industrial or products like human haemoglobih, industrial or of vaccines, healthcare products like human haemoglobibh, industrial or consumption include maize, millet, sorghum, sugar cane, rice, wheat, bariey, oat, rye or turf grass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, leader sequence and a downstream box element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green fluorescent protein; GFP; aadA; protein expression; vaccine;
haemoglobin; enzyme; psbA; T7 phage gene 10; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
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Best Local Similarity 100.0%; Score 182; DB 21;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 182; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 182 BP; 49 A; 34 C; 56 G; 43 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of DNA construct FLARE11-S3.
                                     (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ61384 standard; DNA; 1961 BP
                                                                                                                                                       Claim 4; Fig 3D; 164pp; English
       99US-0131611.
99US-0138764.
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                                                               Maliga P, Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Unidentified.
Aequorea victoria.
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GC 182
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         29-APR-1999;
11-JUN-1999;
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The present sequence represents a DNA construct of the invention.

The specification describes recombinant DNA constructs for expressing the specification describes recombinant DNA constructs for expressing constructs comprises 5' regulatory region which includes a promoter constructs comprise 5' regulatory region which includes a promoter constructs comprises of the heterologous protein. The climeric regulatory construct a coding region of the heterologous protein. The climeric regulatory city of the DNA constructs are used for producing transformed the DNA construct. The DNA constructs are used for producing transformed component and dicor plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with constructs industrial or pharmaceutical importance, including production convections with the constructs in the plants which can be transformed with the constructs household enzymes. Plants which can be transformed with the constructs the barley, oat, rye or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element
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/166..1954
/*tag= d
/note= "psbA region"
                                                              /*tag= a
/note= "T7 phage gene 10 downstream box"
218.1001
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Location/Qualifiers
7..176
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98US-0112257.
99US-0131611.
99US-0138764.
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15-DEC-1998;
29-APR-1999;
11-JUN-1999;
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GC 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element
                                                                                                                                                                                                       aadA; protein expression; vaccine; haemoglobin; enzyme; psbA;
T7 phage gene 10; downstream box; green fluorescent protein; ss.
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/*tag= d
/note= "T7 phage gene 10 downstream box"
3877..5263
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1904..2092
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/note= "psbA sequence"
2103..2823
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                                                                                                                                                                           Nucleotide sequence of plasmid pMSK49.
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1..1880
                                                                        386/c
AAZ61386 standard; DNA; 5263 BP.
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98US-0112257.
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29-APR-1999;
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GC 182
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                                                                                                                                                                                                                                                     Synthetic
                                                                                                                AAZ61386;
                                                      AAZ61386/c
ID
             181
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Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
Prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
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of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
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0
                                                                                                                                 Length 5263;
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                                                                           0 other;
                                                                                                                                                                                  Indels
                                                                           Sequence 5263 BP; 1377 A; 1326 C; 1144 G; 1416 T;
                                                                                                                            Query Match 100.0%; Score 182; DB 21; Best Local Similarity 100.0%; Pred. No. 4.2e-50; Matches 182; Conservative 0; Mismatches 0;
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/note= "Prrn plastid promoter"
/41..144
/*tag= b
/note= "Shine-Dalgarno sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 3D; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ61374 standard; DNA; 182 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maliga P, Kuroda H, Khan MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0095163.
98US-0095167.
98US-0112257.
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/*tag=
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03-AUG-1998;
15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GC 3676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1999;
11-JUN-1999;
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29-APR-1999;
11-JUN-1999;
                                                           Maliga P,
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AAZ88175
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  The present sequence represents a chimeric plastid rRNA operon congervity (Prrn) promoter with the T7 phage gene and Escherichia coll comega-type (Prrn) promoter with the T7 phage gene and Escherichia coll comega-type (Prrn) promoter is used, as a 5' regulatory constructs for expressing sequence, to produce recombinant DNA constructs for expressing the plastids of higher plants. The DNA heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter constructs comprise and advanstream box element operably linked constructs and edwinstream than the contact regulatory to a coding region of the heterologous protein. The chimeric regulatory credion enhances translational efficiency of an mRNA molecule encoded by reducine cannotes translational efficiency of an entry and dicot plants having high levels of heterologous protein capromomic, industrial or pharmaceutical importance, including production agronomic, industrial or pharmaceutical importance, including production capronomic, industrial or pharmaceutical importance includential or protein include maize, millet, sorghum, sugar cane, rice, cof the invention include maize, millet, sorghum, sugar cane, rice, cof weat, barley, out, rye or turf grass.
                                                                                                                                                                                                                                                                    ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
                                                                                                                                                                                                                                                                                                                                      121 ATTIGITIAACTITAAGAAGGAGATATACATATGGCAAGCATGACTGGTGGACACGCTA 180
                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                             DB_21; Length 182;
                                                                                                                                                                                                                                               Query Match

90.3%; Score 164.4; DB 21; Length
Best Local Similarity 94.0%; Pred. No. 8.2e-45;
Matches 171; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of chimeric promoter PrrnLT7g10-DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
7.89
7.89
7.40
7.410
141.14
141.14
7.410
7.410
7.410
7.410
7.410
                                                                                                                                                                                                                          Sequence 182 BP; 47 A; 38 C; 52 G; 45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ61375 standard; DNA; 161 BP.
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98US-0095167.
98US-0112257.
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03-AUG-1998;
15-DEC-1998;
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|GC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                              GC 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
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The present sequence represents a chimmeric plastid rRNA operon

CC omega-type (Prrn) promoter with the T7 phage gene and a synthetic

C omega-type (Prrn) promoter with the T7 phage gene and a synthetic

CC demonstream box. The chimmeric promoter is used, as a 5, regulatory

CC sequence, to produce recombinant DNA constructs for expressing

CC constructs comprise a 5' regulatory region which includes a promoter

CC constructs comprise a 5' regulatory region which includes a promoter

CC clement, a leader sequence and downstream box element operably linked

CC clement, a leader sequence and downstream box element operably linked

CC clement, a leader sequence and downstream box element operably linked

CC clement, a leader sequence and downstream box element operably linked

CC clement, a leader sequence and downstread levels of heterologous protein

CC construct. The DNA constructs are used for producing production

CC construct in they can be used to drive expression of proteins with

CC constructs having high levels of heterologous protein

CC consecution industrial or pharmaceutical importance, including production

CC draccines, healthcare products like human haemoglobin, industrial or

CC consecution include maize, millet, sorghum, sugar cane, rice,

CC the invention include maize, millet, sorghum, sugar cane, rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tobacco; ribosome binding site; aprotinin; herbicide tolerance; plastid; human growth hormone; insulin; ds.
                                                                                                                                                                                                                               New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGGGGCAGGGATGGCTATATTTCTGGGAGGGAGCCACAACGGTTTCCCACTAGAAATA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161 BP; 43 A; 30 C; 48 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prrn/G10L fusion nucleic acid sequence.
                                                                           (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ88175 standard; DNA; 168 BP.
                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Fig 3D; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US15472.
                                                                                                                                               Khan MS
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99US-0131611.
99US-0138764.
                                                                                                                                                   Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200003022-A2.
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Synthetic.
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26-JUN-2000; 2000WO-US18096.
WO200104327-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF57902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                          The present invention describes a construct (I) comprising a plant plastid promoter region, a DNA sequence capable of conferring herbicide colerance in the plant cell and a transcription termination region operably joined in the 5'-3' direction. (I) is useful for producing operably joined in the 5'-3' direction. (I) is useful for producing cherbicide tolerance is useful for selecting cells transformed with (I) and the herbicide tolerance is useful for selecting cells transformed with (I) and the herbicide tolerance or but sequences expression construct is useful for directing expression of DNA sequences concoding enzymes involved in herbicide tolerance or for producing pharmaceutical proteins e.g. human growth hormone, aprothin, insulin or insulin precursors. Transplastomic plants have high level of tolerance to herbicides. Protein levels obtained from plastid expression constructs of the expression constructs. By including targeting sequences, is found to be higher than from nuclear expression constructs. By including targeting sequences, then nuclear expression constructs. By including targeting sequences, the expressed proteins can be targeted to particular suborganellar regions for e.g. thylakoid membrane, which facilitates increased oxidative stability and proper protein folding. Insect or disease constructs. The present sequence represents a Prin/G10L fusion nucleic acid sequence, which is used in an example from the present invention of for the production of expression constructs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CAGGGATGGCTATATTTCTGGGAGGGACCACACGGTTTCCCCACTAGAAATAATTTTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 GCTCCCCGCCGTCGTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGG 82
                                                                                                                              New construct useful for producing herbicide tolerance in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GCTCCCCCCCCCGCCGTCGTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
                                                                 Stalker DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.1%; Score 111.2; DB 21; Length 88.7%; Pred. No. 3.8e-27; ive 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of Prrn/G10L promoter/RBS hybrid.
                                                                                                                                           for directing production of pharmaceutical proteins
                                                                Nehra N, Schaaf DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant plastid; herbicide tolerance; EPSPS protein;
G10L ribosome binding site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 6; 62pp; English.
                                                                McBride KE,
           98US-0113257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF25352 standard; DNA; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 133; Conservative
                                                                                                    WPI; 2000-147617/13.
                                     (CALJ ) CALGENE LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                             Hajdukiewicz P,
Staub JM, Ye G;
           10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2001
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The specification describes a construct comprising a promoter functional in a plant plastid, a DNA sequence capable of conferring tolerance in a plant cell to at least one herbicide compound when the DNA sequence is transcribed in plant cell plastids, and a transcription termination region, in the 5'-3' direction of transcription. The construct is useful for producing tolerance of a herbicide in a plant cell. The construct is also useful for enhancing expression of a wide variety of genes, both eukaryotic and prokaryotic, in plant plastids. It is useful for genetic engineering of plant cells and which provide for enhanced expression of EPSPS proteins or hGH protein in plant cell plastids. The present sequence represents a hybrid comprising plastid 16S ribosomal RNA operon, and a synthetic Glür ribosome binding site (RBS). The hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel constructs for expressing herbicide tolerance genes in plant cell plastids, comprises a promoter functional in plant plastid, a DNA sequence conferring herbicide tolerance and transcription terminator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green fluorescent protein; GFP; translational fusion; gene expression; herbicide tolerance; pharmaceutical protein; disease resistance; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.1%; Score 111.2; DB 22; Length
88.7%; Pred. No. 3.8e-27;
ive 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is used to produce constructs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prrn/G10L promoter/RBS hybrid coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 TITAACTTTAAGAAGGAGATATACCCATGG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITAACTITAAGAAGGAGATATACATATGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 6; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF57902 standard; DNA; 168 BP
                                                                         10-JUL-2000; 2000WO-US18727.
                                                                                                                                               99US-0351123
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-138356/14.
                                                                                                                                                                                                                        (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200104331-A2.
                                                                                                                                                                                                                                                                                              Hajdukiewicz P;
                                                                                                                                               .0-JUL-1999;
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18-JAN-2001
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The present sequence represents a chimeric plastid rRNA operon omega-type (Prrn) promoter with atpB translation control sequences, without a downstream box. The chimeric promoter is used, as a 5' required, to produce recombinant DNA constructs for expressing required; to produce recombinant DNA constructs for expressing neterologous proteins in the plastida of higher plants. The DNA heterologous proteins a 5' requilatory region which includes a promoter constructs comprises a 5' requilatory region within includes a promoter constructs comprises and a downstream box element operably linked element, a leader sequence and a downstream box element operably linked clement, a leader sequence and a downstream box element operably linked the DNA construct. The DNA constructs are used for producing transformed the DNA constructs are used for producing transformed characteric products and dicor plants having high levels of heterologous protein with agreening, industrial or pharmaceutical importance, including production agronomic, industrial or pharmaceutical importance including production of vaccines, healthcare products like human heamoglobin, industrial or for the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or tuf grass.
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                                                                                                                                                                                New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGGGGCAGGGATGGCTATATTTCTGGGAGGGAGACCACAACGGTTTCCCACTAGAAATA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of chimeric promoter PrrnLatpB+DBwt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
51.4%; Score 93.6; DB 21;
Best Local Similarity 75.0%; Pred. No. 2.8e-21;
Matches 117; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 191 BP; 52 A; 32 C; 48 G; 59 T; 0 other;
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"Prrn plastid promoter"
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                                                                                     (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
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                                                                                                                         Khan MS
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98US-0095167.
98US-0112257.
99US-0131611.
99US-0138764.
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/*tag=
/note=
                                                                                                                         Maliga P, Kuroda H,
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    03-AUG-1998;
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29-APR-1999;
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                                                                                                                                                                                                                                                                                     The present invention describes a construct comprising a promoter region, a DNA sequence encoding at least the first 5 amino acids of green the first 5 amino acids of green and a transcription (FP), a DNA sequence encoding a protein of interest and a transcription termination region. Constructs of this type have been shown to enhance gene expression, and they can be used in plants to confer herbicide tolerance, disease resistance and the ability to produce pharmaceutically important proteins on the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; prrn promoter; atpB; protein expression; vaccine; enzyme; ss.
                                                                                                                                                                New constructs encoding translational fusion of 14 amino acids derived from green fluorescent protein for enhancing desired protein (5-enolpyruvylshikimate-3-phosphate synthase) expression in plant cells
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/note* "Shine-Dalgarno sequence"
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7.89
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/note- "Prrn plastid promoter"
114..116
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                                  99US-0351124
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                                                                        (CALJ ) CALGENE LLC
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15-DEC-1998;
29-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a chimeric plastid rRNA operon conga-type (Prrn) promoter with atpB translation control sequences and a wild type downstream box. The chimeric promoter is used, as a 5' regulatory sequence, to produce recombinate DNA constructs for expressing thererologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter calement, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production confuseshold enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
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Pred. No. 3e-21;
0; Mismatches 39;
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                     /*tag= b
/note= "Shine-Dalgarno sequence"
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99US-0131611.
99US-0138764.
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Best Local Similarity 75.0%;
Matches 117; Conservative
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114..116
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The present sequence represents a chimeric plastid rRNA operon omega-type (Prrn) promoter with atpB translation control sequences and a mutated downstream box. The chimeric promoter is used, as a 5' calculatory sequence, to produce recombinant DNA constructs for expressing heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed consort and dioct plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production for vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
                                                                        Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; atpB; protein expression; vaccine; enzyme; ss.
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Pred. No. 3e-21;
0; Mismatches 39; Indels
Nucleotide sequence of chimeric promoter PrrnLatpB+DBm
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/note= "Shine-Dalgarno sequence"
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Best Local Similarity 75.0%;
Matches 117; Conservative (
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The present sequence represents a DNA construct of the invention. The specification describes recombinant DNA constructs for expressing heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5' regulatory region which includes a promoter a leader sequence and a domastream box element, or element, or a leader sequence and a domastream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of an mRNA molecule encoded by the DNA construct. The DNA constructs are used for producing transformed monocot and dicot plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with agronomic, industrial or pharmacoutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or vaccines, healthcare products like human haemoglobin, industrial or the invention include malze, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA constructs, for expressing high levels of heterologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element .
                                                                                                                                                                                                                           Green fluorescent protein; GFP; aadA; aptB; protein expression; vaccine;
haemoqlobin; enzyme; pSbA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93.6; DB 21; Length 1985; Pred. No. 6.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag by horse "aadA sequence"
//tag c //tag d //tag d
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                                                                                                                                                                  Nucleotide sequence of DNA construct FLARE16-S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 .221
/*tag
/note= "atpB downstream box"
228 .1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 30; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maliga P, Kuroda H, Khan MS;
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75.0%;
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98US-0095167.
98US-0112257.
99US-0131611.
AAZ61382 standard; DNA; 1985
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                                                                                                                 (first entry)
                                                                                                                                                                                                                                                            haemoglobin; enzyme; psbA;
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                                                                                                                                                                                                                                                                                                              Synthetic.
Unidentified.
Aequorea victoria.
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15-DEC-1998;
29-APR-1999;
11-JUN-1999;
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misc_feature
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                                                        AAZ61382;
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                                                                                                                                                                                                                                                                                                                        DNA fragment designed for CRE-induced expression of recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in an example illustrating an invention relating to a method for manipulating the genome of higher plants. The method involves selecting plant cells expressing proteins encoded by a DNA construct having a nucleic acid encoding a marker, excision sites and plastid targeting sequence for homologous recombination into a plastid genome at a target sequence. The method is useful for removing heterologous sequences from the plastid genome, such as selectable marker genes following successful isotation of transformed progeny, and for removing endogenous genes associated with maie sterility, clp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGCTCGCTCCCCCCCCCCCTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Removing target nucleic acid sequences e.g. selectable marker genes, genes involved in plant cell metabolism, growth development and fertility from plastid genomes, by Cre-mediated site specific recombination -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%; Score 93.6; DB 22; Length 1049; llarity 75.0%; Pred, No. 5.4e-21; Conservative 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1049 BP; 269 A; 235 C; 282 G; 263 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATTTTGTTTAACTTTTAAGAAGGAGATATACATATGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TATTTTAAATTCGATAATTTTGCAAAAACATTTCG 156
                                                                                                                                                                                                                                                                                                                                                                             CRE recombinase; plastid genome manipulation; site-specific recombination; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
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                                                                                                                                                     AAF81268 standard; DNA; 1049 BP
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Matches 117; Conserv
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Query Match Best Local Similarity

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15-DEC-1998;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                               Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; psbB; protein expression; vaccine; enzyme; ss.
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                                                                                                        61 AGGGGGCAGGGATGGCTATATTTCTGGGAGAATTAACCGATCGACGTGCAAGCGGACATT 120
                                                                                        AGGGGGCAGGGATGCCTATATTTCTGGGAGGGAGACCACACGGTTTCCCACTAGAAATA 120
                                                           9
 Gaps
                             GAGCTCGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60
                                                        1 GAGCTCGCTCCCCCGCCGTCGTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTG
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0
39; Indels
                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of chimeric promoter PrrnLpsbB-DB.
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/*tag= b
/note= "Shine-Dalgarno sequence"
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/note= "Prrn plastid promoter"
                                                                                                                                                    ATTITIGITIAACTITAAGAAGGAGATATACATATGG 156
                                                                                                                                                                                121 TATTTTAAATTCGATAATTTTTGCAAAAACATTTCG 156
0; Mismatches
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98US-0095167.
98US-0112257.
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Matches 117; Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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expression. They can be used to drive expression of proteins with agronomic, industrial or pharmaceutical importance, including production of vaccines, hearthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
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Prrn promoter; psbA; protein expression; vaccine; enzyme; ss.
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                                                                                                                                                                                                                                                                Length 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.2; DB 21;
Pred. No. 7.6e-21;
0; Mismatches 8;
                                                                                                                                                                                                          Sequence 153 BP; 36 A; 27 C; 47 G; 43 T; 0 other;
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/*tag= b
/note= "Shine-Dalgarno sequence"
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/note= "Prrn plastid promoter"
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98US-0112257.
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ilarity 92.4%;
Conservative
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es 97; Conserv
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Search completed: December 15, 2002, 00:32:45 Job time: 311 secs

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         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-193-853-2
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US-09-202-316-4
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-09-202-316-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-283-419-3
US-08-189-256A-
                                                                                                                                                                                  441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                - nucleic search, using sw model
                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                            US-09-762-105-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the score greater than and is derived b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                                                      Perfect score:
                                                  OM nucleic
                                                                                                                                                                                  Searched:
                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                Database
                                                                     Run on:
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METHODS FOR PRODUCING CYTOPLASMIC MALE STERILITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
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                                                                    Sequence 7, My Sequence 7, My Sequence 7, My Sequence 7, My Sequence 13, My Sequence 13, My Sequence 9, My Sequence 9, My Sequence 1, My Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCCCCCCCGTCGTTCAATGAATGGATAAGAGGCTCGTGGGGATTGACGTGAGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, A
Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dann, Dorfman, Herrell and Skillman, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89.6; DB 1;
Pred. No. 1.3e-21;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rutgers University
US-09-193-853-3
US-08-040-753-1
US-08-096-182A-7
US-08-096-182A-7
US-08-877-109-7
US-08-217-360-7
US-08-217-360-17
US-08-217-360-17
US-08-327-028-9
US-09-337-028-9
US-09-337-028-9
US-09-338-33-1
US-08-902-623-44
US-08-902-623-44
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US-08-929-967-3
US-09-265-919-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1601 Market Street, Suite 720 CITY: Philadelphia STATE: PA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-MAR-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: REED, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PETENT RE-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Ve
CURENT APPLICATION NUMBER: US/08/217,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-08-277-360-16.
Sequence 16, Application US/08217360
Patent No. 5530191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: Ru
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (215)563-4044
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.28;
78.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 171 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 49.2
Best Local Similarity 78.3
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MALIGA, Pal
TITLE OF INVENTION: METI
TITLE OF INVENTION: MALI
TITLE OF INVENTION: SEEI
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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us-09-193-853-25
sequence 25, Application Us/09193853
sequence 25, Applicant walled. Pallson, Dallson, Dallson, Dallson, Dallson, Loria Applicant Ranevski, Ivan
Applicant Ranevski, Ivan
Applicant Ranevski, Ivan
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSED: Dan, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
6 GCTCCCCCCCCTCCATCAATGAGATGGATAAGAGGCTCGTGGGATTGACGTGAGGGG 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 CAGGGATGGCTATATTTCTGGGAGGGAGCCACACAAGGGTTTCCC 110
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ZIP: 19103-2307

ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATION DATA:
CURRENT APPLICATION DATA:
PRING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/189,256
APPLICATION NUMBER: 08/189,256
                                                      67 CAGGGATGCCTATATTTCTGGGAGGGAGACCACAACGGTTTCCC 110
                                                                                        APPLICATION .....
FILING DATE:
PRIOR APPLICATION NUMBER: US 07/518,763
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAX-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Jandet B. 36,252
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4104
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH 129 base pairs
TYPE: Unucleic acid
TYPE: INDICATION SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLLGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ANTI-SENSE:
US-09-193-853-25
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Sequence 25, Application US/08189256A

Petent No. 5877402

Petent No. 587402

APPLICANT: Stabb. Jeffrey

APPLICANT: Allson. Lord No. 1897402

APPLICANT: Allson. Day Compatible Proteins Therein

APPLICANT: Carrer, Helaine

APPLICANT: Day Carrer, Herrell and Skillman

ANDERSORE OF SECURDES: Expressing Recombinant Proteins Therein

NUBBER OF SECURDES: Expressing Recombinant Proteins Therein

ANDERSORE OF SECURDES: Expressing Recombinant Proteins Therein

ANDERSORE OF SECURDES: Expressing Recombinant Proteins Therein

STATE: Philadelphia

STATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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0
                                          Score 86.4; DB 2; Length 129;
Pred. No. 1.58-20;
0; Mismatches 11; Indels (
                                                                                                                                                                                                                   105 TTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATAC 150
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 89.4%;
Matches 93; Conservative
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US-08-189-256A-25
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Gaps

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APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Stabb, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ 1D NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 140 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Reed, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
Matches 92; Conserv
                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-09-193-853-19
Patent No. 6388168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-189-256A-26
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                                                                                                                                                                    APPLICANT: Svab, Jorfand APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Loria A
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: Tansveski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
MUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 47.3%; Score 86; DB 2; Length 140; 1 Similarity 90.2%; Pred. No. 2.1e-20; 92; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARES: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A FILING DATE: 31-JAN-1994
FILING DATE: 31-JAN-1994
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: REGGIAGATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGGATGGCTATATTCTGGGAGGGAGACCACACGGTTTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 Sequence 19, Application US/08189256A Patent No. 5877402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-193-853-19
: Sequence 19, Application US/09193853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                               APPLICANT: Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity Matches 92; Conserv
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                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-189-256A-19
                                                         US-08-189-256A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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APPLICAMIT: SAIDS, Deffery
APPLICAMIT: SAIDS, JOETE
APPLICAMIT: ALLISON, LOIR A.
APPLICAMIT: APPLICA
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RESULT 8
US-08-189-256A-18
Sequence 18, Application US/08189256A
Sequence 18, Application US/08189256A
Setent No. 5877402
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MCLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3
Query Match
Best Local Similarity 90.2
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-09-193-853-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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US-09-193-653-26
US-09-193-653-26
Sequence 26, Application US/09193853
Sequence 26, Application
Sequence 26, Application
Sequence 26, Application
APPLICANT: Waliga, Pal
APPLICANT: Staub, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Allison, Lori A-
APPLICANT: Carrer, Helaine
APPLICANT: Carrer, Helaine
APPLICANT: Helaine
APPLICANT: Wannion: DNA Constructs and Methods for Stably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
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Best Local Similarity 90.2%; Pred. No. 2.2e-20;
Matches 92; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: PA
CYUNTRY: USA
ZIP: 19103-2307
ZIP: 19103-2307
ZIP: 19103-2307
COMPUTER: LEB PC COMPACIBLE
COMPUTER: ELEB PC COMPACIBLE
COMPUTER: THE PC COMPACIBLE
APPLICATION NUMBER: US COF111,398
FILING DATE: 25-AGC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US COF518,763
FILING DATE: 25-AGC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 35,252
FILING DATE: COMPACIBLE
COMPUNICATION NUMBER: 36,252
FILING DATE: COMPACIBLE
NUMBER: THE PC CARRCTERESTICS:
CELECOMMUNICATION IN NO: 26:
SEQUENCE CARRCTERESTICS:
CENTRAL CARRCTERESTICS:
CENTRAL CARRCTERESTICS:
CENTRAL CARRCTERESTICS:
COMPUTER TOLE NO
COLOGY: LINEAR GENOLO
COMPUTER TOLE
COMPUTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and NUMBER OF SEQUENCES: 47

NUMBER OF SEQUENCES: 47

COMPRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Dann, Dorferet Suite 720

COMPUTED FOR THIS STREET: Philadelphia STARE: PA

COMPUTER TEADABLE FORM: COMPATIBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE FORM: MEDIUM TYPE: PACHICATION DATA: APPLICATION UNBER: US/09/193,853

FILING DATE: PROJECATION DATA: APPLICATION NUMBER: US/09/193,853

FILING DATE: PROJECATION DATA: PROJECATION NUMBER: US/09/193,853

FILING DATE: PROPEMATION NUMBER: US/09/193,853

FILING DATE: PROPEMATION: PROPEMATION: NUMBER: US/09/193,853

FILING DATE: PROPEMATION: THORMATION: NAME: Reed, Janet E. S. S. SETTING DATE: THE COMPATION NUMBER: US/09/193,853

FILING DATE: PROPEMATION UNMBER: US/09/193,853

FILING DATE: PROPEMATION UNMBER: US/09/193,853

FILING DATE: THORMATION: THORMATION: NAME: Reed, Janet E. S. S. SETTING DATE: TELECOMMUNICATION INFORMATION: SEQUENCE SEQUENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Waliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Soutener, Lori A.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Ranevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
TITLE OF INVENTION: APPLICANT AND APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 CAGGGATGGCTATATTTCTGGGAGGGAGCCACACACGGTTTC 108
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GENERAL INFORMATION:

APPLICANT: Maliga, Pal
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Alison, Lori A.
APPLICANT: Alison, Lori A.
APPLICANT: Ranevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GCTCCCCCCCCCGTCGTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Dann, Dorfman, Herrell and Skillman: 1601 Market Street Suite 720 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 85.4; DB 4;
Pred. No. 3.5e-20;
0; Mismatches 1;
                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
FILING DATE:
FRICK APPLICATION NUMBER: 05/518,763
APPLICATION NUMBER: 05/518,763
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEFRONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 CAGGGATGGCTATATTTCTGGGAGGGA 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.9%;
Best Local Similarity 98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-189-256A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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APPLICANT: Maliga, Pal
APPLICANT: Staub, Jorfar
APPLICANT: Staub, Jorfar
APPLICANT: Staub, Jorday V.
APPLICANT: Allison, Lori A.
APPLICANT: Caurrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 GCTCCCCCCCCCCTCCATCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 GCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.9%; Score 85.4; DB 2; Length 161; nilarity 98.9%; Pred. No. 3.5e-20; Conservative 0; Mismatches 1; Indels
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIE: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Dann, Dorfman, Herrell and Skillman
: 1601 Market Street Suite 720
Philadelphia
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 433
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INCOMMATION:
TELECHMUNICATION INCOMMATION:
TELECHMUNICATION INCOMMATION:
TELECHMUNICATION: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CAGGGATGCCTATATTTCTGGGAGGGA 93
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         1601 Market Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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CORRESPONDENCE ADDRESS:
                             Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 86; Conserv
                                                                                                 19103-2307
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ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-189-256A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-193-853-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: TBM PC compatible

OFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,853
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATE: US 07/518,763
APPLICATION NUMBER: US 07/518,763
ATTORNEY: US 01-MAY-1990
ATTORNEY: US 01-MAY-1990
ATTORNEY: US 01-MAY-1990
ATTORNEY: (215) 563-4400
TELECOMMUNICATION NUMBER: 36,252
TELENOMMINICATION 18FORMATION:
TELEMENT: 1815 base pairs
TELENOMMINICATION NOT SECONOMMINICATION NOT SECONOMMINICATION NOT SECONOMMINICATION NOT SECONOMMINICATION SECONOMINICATION SECONOMINICATION SECONOMINICATION SECONOMINICATIO
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Best Local Similarity 98.9
Matches 86; Conservative
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PRIOR APPLICATION NUMBER: 06/189,256
FILTHE DATE APPLICATION NUMBER: 106/189,266
APPLICATION NUMBER: 106/189,763
APPLICATION NUMBER: 106/189,763
APPLICATION NUMBER: 106/189,763
APPLICATION NUMBER: 106/189,763
APPLICATION NUMBER: 106/189,764
APPLICATION NUMBER: 106/189,766
APPLICATION NUMBER: 106/189,766
APPLICATION NUMBER: 106/189,766
APPLICATION NUMBER: 106/189,766
APPLICATION NUMBER: 106/189,769
APPLICATION N
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0;

Gaps

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7 GCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bogosian, Gregg
APPLICANT: O'Neal, Julia P.
APPLICANT: Staub, Jofffrey M.
TITLE OF INVENTION: Bacterial Expression Systems Based on Plastid or TITLE OF INVENTION: Mitochondrial Promoter Combinations
FILE REFERENCE: MOPV040---
CURRENT APPLICATION NUMBER: US/09/283,419A
CURRENT FILING DATE: 1999-04-01
EARLIER FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                              Indels
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Pred. No. 3.7e-20;
0; Mismatches 1;
                                                                                                                                                                                                                                                     Score 85.4; DB 4;
Pred. No. 3.6e-20;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CAGGGATGCTATATTTCTGGGAGCGA 88
                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGGATGGCTATATTTCTGGGAGGGA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08189256A

Patent No. 5877402

GENERAL INFORMATION:

APPLICANT: Waliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-283-419-3; Sequence 3, Application US/09283419A; Patent No. 6218145
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Svab, Zora
Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
Kanevski, Ivan
                                                                                                                                                                                                                                                  46.98;
98.98;
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Best Local Similarity 98.9%;
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-283-419-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                     Query Match 46.9
Best Local Similarity 98.9
Matches 86; Conservative
                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       õ
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US-09-193-853-2
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APPLICANT:
APPLICANT:
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APPLICANT: Stabb, Joffrey
APPLICANT: Stabb, Joffrey
APPLICANT: Soubenko, oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 60
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                                                                                                                                                                                                                                                                                                                                                       Length 168;
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                                                                                                                                                                                                                                                                                                                                                     ch 46.9%; Score 85.4; DB 2; 11 Similarity 98.9%; Pred. No. 3.6e-20; B6; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/193,853
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
               NAME: Reed, Janet E.
REGISTRATION UNDREE: 36.252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09193853
Patent No. 6388168
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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Best Local Similarity
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ZIP: 19103-2307
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                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-189-256A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-193-853-2
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Gaps

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TITLE OF INVENTION: DNA CONSTRUCTS and Methods for Stably
TITLE OF INVENTION: Transforming plastids of Multicellular
TITLE OF INVENTION: Transforming plastids of Multicellular
NUMBER OF SEQUENCES: 47
CORRESPONDENCES: 47
CORRES
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46.9%; Score 85.4; DB 2; Length 258;
Best Local Similarity 98.9%; Pred. No. 4.3e-20;
Matches 86; Conservative 0; Mismatches 1; Indels
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US-08-189-256A-24
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Search completed: December 15, 2002, 02:07:54 Job time : 68 secs

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817.885 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                    355320 segs, 197730502 residues
                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Published_Applications_NA:*

Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appli,			۲.	, Appl	Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	Appli	Appli
	ជ		2	12	6	51	49	47	53	55	57	59	61	63	65	43	45	67	5,	ω,
	Description	Sequence 1,	Sequence 2,	Sequence 12	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		US-09-843-324A-1	US-09-843-324A-2	US-10-085-476-12	JS-09-813-718-9	JS-09-987-107-51	JS-09-987-107-49	-09-987-107-47	US-09-987-107-53	-09-987-107-55	JS-09-987-107-57	JS-09-987-107-59	US-09-987-107-61	-09-987-107-63	JS-09-987-107-65	JS-09-987-107-43	JS-09-987-107-45	-09-987-107-67	US-09-813-718-5	US-09-813-718-3
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	DB	10	10	σ	σ	6	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ
æ	Query Match Length DB	202	244	399	5018	1057	1088	1217	1217	1238	1238	1238	1241	1241	1241	1282	1285	1301	4100	4682
	Query Match	42.7	42.7	38.0	37.1	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.7	36.5
	Score	77.8	77.8	69.2	67.6	8.99	66.8	66.8	8.99	66.8	8.99	8.99	8.99	8.99	9.99	8.99	66.8	8.99	8.99	66.4
	Result No.	п	2	က	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18	19

Sequence 7, Appli Sequence 11, Appli Sequence 11, Appli Sequence 5, Appli Sequence 13, Appli Sequence 13, Appli Sequence 17, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appli Sequence 14, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	7 8 2 2 8 2 4 8 2 8 2 8 2 8 2 8 2 8 2 8 2
US-09-813-718 US-09-813-718 US-09-813-718 US-09-976-297 US-09-916-297 US-09-813-718 US-09-813-718 US-09-838-71 US-09-838-71 US-09-838-71 US-09-933-72 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-91 US-09-929-94 US-09-929-94	US-09-736-457-785 US-09-902-941-785 US-09-736-457-784 US-09-902-941-784
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4682 656 656 4742 4742 4742 4742 4741 174 118 630 630 630 630 630 630 630	5502 5502 6353 6353
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0 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	4 4 4 4 5 4 5 3 5

ALIGNMENTS

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                                                   GENERAL INFORMATION:
APPLICANT: Staub, Jeffrey
APPLICANT: Te, Gangning
APPLICANT: Broyles, Debra
TITLE OF INVENTION: Method for the transformation of plant cell plastids
FILE REFERENCE: 12869/W0
CURRENT APPLICATION NUMBER: US/09/843,324A
CURRENT FILING DATE: 2001-04-25
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 CCGCCGTCGTTCAATGAAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGGCAGGGA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 CCCCCGTCGTTCAATGAAAAGAGGCTCGTGGGATTGACGTGAGGGGGGGAA 70
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.7%; Score 77.8; DB 10; Best Local Similarity 97.5%; Pred. No. 3.1e-16; Matches 79; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-843-324A-2
Sequence 2, Application US/09843324A
Patent No. US20020042934A1
GENERAL INFORMATION:
                  ; Sequence 1, Application US/09843324A
; Patent No. US20020042934A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TGGCTATATTTCTGGGAGCGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 TGGCTATATTTCTGGGAGGGA 93
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Version 3.0
SEQ ID NO 1
LENGTH: 202
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
US-09-843-324A-1
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Sequence to Application US/09813718
Sequence to No. US20020182666A1
SCREENAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: He Regulation of Anglogenesis
FILE REFERENCE: 00-221
FULE REFERENCE: 00-221
CUBRENT APPLICATION WUMBER: US/09/813,718
CUBRENT PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 5018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 AGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATAT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 AGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATAT 148
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36.7%; Score 66.8; DB 9; Length 1057;
Best Local Similarity 97.1%; Pred. No. 2.4e-12;
Matches 68; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KET: CDS

LOCATION: (3428)..(4879)

OTHER INFORMATION: Description of Artificial Sequence: human

CTHER INFORMATION: full-length TrpRS in pET20B

US-09-813-718-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KESULT 5
US-09-987-107-51
Squence 51, Application US/09987107
Patent No. US20020156007A1
CENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOCIETOPROTEINS APLICANT:
CURRENT APPLICANT: APOLITOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-15
SROFTWARE: PRIOR FILING DATE: 2001-01-15
SROFTWARE: PRIOR PRIOR SEC ID NOS: 911-10
NUMBER OF SEC ID NOS: 911-10
SEC ID NO 51
LENGTH: 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

37.1%; Score 67.6; DB 9;
Best Local Similarity 94.6%; Pred. No. 2.6e-12;
Matches 70; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: PT7 H6 Fx Cys-Apo Al plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LOCATION: (100)..(882)
COTHER INFORMATION:
US-09-987-107-51
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Sequence 12, Application US/10085476

Fatent No. US200201647221

GENERAL INFORMATION:

APPLICANT: Tomei, Licia

APPLICANT: Tomei, Licia

APPLICANT: Tomei, Licia

TITLE OF INVENTION: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL

TITLE OF INVENTION: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL

TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)

FILE REFRENCE: ITO002PCA

CURRENT APPLICATION NUMBER: US/10/085,476

CURRENT FILING DATE: 1996-03-23

PRIOR PILING DATE: 1996-03-23

PRIOR APPLICATION NUMBER: RW55A00343

PRIOR FILING DATE: 1996-05-24

PRIOR FILING DATE: 1996-05-24

PRIOR FILING DATE: 1996-05-24

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LEADLY: 399
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APPLICANT: Staub, Jeffrey
APPLICANT: Ye, Guanghing
APPLICANT: Ye, Guanghing
APPLICANT: Ye, Guanghing
APPLICANT: Broyles, Debra
TITLE OF INVENTION: Method for the transformation of plant cell plastids
FILE REFERENCE: 15865/WO
CURRENT APPLICATION NUMBER: US/09/843,324A
CURRENT FILING DATE: 2001-04-25
FRIOR PAPLICATION NUMBER: 60/199,774
PRIOR FILING DATE: 2000
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEG ID NO 2
LENGTH: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Best Local Similarity 97.5%; Pred. No. 3.4e-16;
Matches 79; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 69.2; DB 9; Length 399; 68.9%; Pred, No. 2.6e-13; Live 20; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic construct US-09-843-324A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TGGCTATATTTCTGGGAGGGA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 TGGCTATATTTCTGGGAGCGA 91
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: RNA
; ORGANISM: Rattus norvegicus
US-10-085-476-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.9%
Matches 51; Conservative
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US-10-085-476-12
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Length 1217;

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89 AGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATAT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.7%; Score 66.8; DB 9; Length 1217; 97.1%; Pred. No. 2.6e-12; Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: PT7H6 Trip-A-Apo Al K9A K15A - AmpR plasmid NAME/KEY: CDS LOCATION: (100)...(1047)
OTHER INFORMATION:
                                          CTHER INFORMATION: pt7 H6 Trip-A-Apo A-1 - AmpR plasmid
NAME/KEY: CDS
LOCATION: (100)..(1047)
COTHER INFORMATION:
US-09-987-107-47
                                                                                                                                                                                   Score 66.8; DB 9;
Pred. No. 2.6e-12;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOCRE
TITLE OF INVENTION: APPLIPOPROTEINS ANALOGUES
FILE OF INVENTION: APPLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR PILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 55, Application US/09987107
Patent No. US/0020156007A1
; GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOSSTRUP, SOTEN
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/09987107 Patent No. US20020156007A1 GENERAL INFORMATION:
                                                                                                                                                                              ch 36.7%;
1 Similarity 97.1%;
68; Conservative C
  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                 Best Local Similarity
Matches 68; Conserv
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Matches 68; Conserv
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                                                                                                                                                                                     Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66.8; DB 9; Length 1
Pred. No. 2.5e-12;
0; Mismatches 2; Indels
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PATENT NO. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSIN, JODAS
APPLICANT: GRAVERSIN, SOLED
ITILE OF INVENTION: APOLITOPROTEINS ANALOGUES
FILE PEFERENCE: GRAVERSINIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT PILING DATE: 2001-11.13
PRIOR FILING DATE: 2001-01.26
PRIOR FILING DATE: 2001-01.26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR PILING DATE: 2001-01-15
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GRAVERSEN, JOOAS
APPLICANT: GRAVERSEN, JOOAS
APPLICANT: GRAVERSEN, JOOAS
TITLE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: DK PAZ001 00057
PRIOR APPLICATION NUMBER: DK PAZ001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SPIOR FILING DATE: 2001-11-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 49
LENGTH: 1088
                                                                                                                                                                                                                           Sequence 49, Application US/09987107 Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.1%;
Matches 68; Conservative 0
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: CDS
; LOCATION: (100)..(918)
; OTHER INFORMATION:
US-09-987-107-49
                                                                                           149 ACATATGGCA 158
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US-09-987-107-47
                                                                                                                                                                              RESULT 6
US-09-987-107-49
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Gaps

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Query Match 36.7%; Score 66.8; DB 9; Length 1238; Best Local Similarity 97.1%; Pred. No. 2.6e-12; Matches 68; Conservative 0; Mismatches 2; Indels 0
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US-09-987-107-61
Sequence 61. Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: APOLICAPPROPERINS
FITLE OF INVENTION: APOLICPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 001-11-13
FRIOR FILLING DATE: 2001-01-26
PRIOR FILLING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 61
LENGTH: 1241
                                                                                          RESULT 11
US-09-987-107-59
Sequence 59, Application US/09987107
Sequence 10 Sequence 1
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 AGGGAGACCACAAAGGTTTCCCTCTAGAAATATTTGTTTAACTTTAAGAAGGAGATT 95
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pT7H6 Trip-A-Fn-Apo Al-final - AmpR plasmid
NAME/KEY: CDS
LOCATION: (100)...(1068)
GOTHER INFORMATION:
US-09-987-107-57
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Pred. No. 2.6e-12;
0; Mismatches 2; Indels 0.
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Sequence 57, Application US/09087107
Sequence 57, Application US/09087107
Sequence 57, Application US/09087107
Sequence 57, Application:

CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PELING DATE: 2001-01-15
PRIOR PELING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PETENTIN VETSION 3.1
SOFTWARE: PETENTIN VETSION 3.1
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Best Local Similarity 97.1%;
Matches 68; Conservative (
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US-09-987-107-57
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PRIOR APPLICATION NUMBER: DK PA2001 00057 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2001-01-10 PRIOR FILING DATE: 2000-11-10 NUMBER OF SEQ ID NOS: 91 SOFFWARE: Patentin version 3.1 SEQ ID NO 65 LENGTH: 1241
                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 97.1%;
Matches 68; Conservative
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Best Local Similarity 97.1%;
Matches 68; Conservative
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; LOCATION: (100)..(1107)
; OTHER INFORMATION:
US-09-987-107-43
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                                                                                                                             Gaps
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                                                                                    Length 1241;
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                                                                                 Score 66.8; DB 9;
Pred. No. 2.6e-12;
0; Mismatches 2;
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US-09-987-107-63
Sequence 63. Application US/09987107
Sequence 63. Application US/09987107
Sequence 63. Application US/09987107
Sequence 63. Application US/09987107
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA SOLEN
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SOFTWARE: PARENTIN NUMBER: DK PA2000 01682
SOFTWARE: PARENTIN NUMBER: DK PA2001
WUMBER OF SEQ ID NOS: 91
SOFTWARE: PARENTIN VEFSION 3.1
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APPLICANT: MOESTRUP, SOCEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
TITLE REPERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR PILICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
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Patent No. US20020156007A1
GENERAL INFORMATION:
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1 Similarity 97.1%;
68; Conservative (
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; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-61
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; LOCATION: (100)..(1071)
; OTHER INFORMATION:
US-09-987-107-63
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                                                                                 Query Match
Best Local 3
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CTHER INFORMATION: pT7H6 Trip-A-Tn-Apo Al final K9AK15A - AmpR plasmid MAME/REY: CDS CATION: (100)..(1071)
COTHER INFORMATION: CDF CATION: COTHER INFORMATION:
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Pred. No. 2.6e-12;
0; Mismatches 2;
                                                                                                                                        Score 66.8; DB 9;
Pred, No. 2.6e-12;
0; Mismatches 2;
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APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
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Patent No. US20020156007A1
GENERAL INFORMATION:
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Search completed: December 15, 2002, 03:13:31 Job time : 92 secs

BOMKE52TR BOHWH29TR

BOGIS47TF

BOGQI49TF

BOHSV92TR BOGKG09TR

Scoring table:

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Run on:

BOMGJ20TR BOMFU26TR BOMIY83TF

BOMLL57TF

BOMGP75TF BOGSU17TF

BOMKZ88TF BOMLI06TF BOMEY 03TF BOHTL37TR LERIR36TR BOHXN88TR

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BH558942 787 bp DNA linear GSS 14-DEC-2001
BOHLZ72TR BOHL Brassica oleraĉea genomic clone BOHLZ72, DNA
                                 BOMFR11TR
LERGI42TR
BOGFU38TR
BOMCM49TR
                                                                                          BOGWR48TF
BOMAG13TR
BOHJD65TR
BOHAC38TF
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qk34a10.b
BOMLA51TR
BOMPL27TR
BOMCZ43TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicacea; Brassica.
1 (bases 1 to 787)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                           BH653681
BH678031
BH678031
BH689289
BH725279
BH725279
BH719545
BH562132
BH562132
BH541747
BH740747
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BH648975 E
AQ967359 I
BH717042 E
BH654995 E
BH694130 E
BH491584 E
BH675079 E
                                           AQ962940
BH537952
BH677595
BH474703
                                                                                           BH646726
BH705426
BH430502
BH493122
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BH662193
BH475597
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BH700638
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BH650341
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9712 Medical Center Drive, Rockville,
1911 301-838-3523
Fax: 301-838-0208
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                      BH474481
BH721450
AQ962940
BH537952
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BH717042
BH654995
BH694130
BH491584
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BH664090
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BH740372
BH718684
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DNA is from a doubled haploid
Seg primer: TR
Class: sheared ends.
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BH558942.1 GI:17810722
 Contact: Chris Town
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sequence.
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
COMMENT
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BH558942
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BH424823 BOHNJ79TR
BH509684 BOHSH07TF
BH472349 BOCIY45TF
BH668002 BOMLN95TF
BH709230 BOMNO33TR
                                                                            December 15, 2002, 00:24:28; Search time 2428 Seconds (without alignments) 1213.994 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                    1 gagetegetececegeegte......tgaetggtggaeaggetage 182
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                                                                                                                                                                                                                                      32308132
         GenCore version 5.1,3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Listing first 45 summaries
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BH509684
BH472349
BH668002
BH709230
                                                         - nucleic search, using sw model
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                                                                                                                                                                            IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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72.6 72.4 72.2 72.2 71.8

BOMLS01TF BOMKP19TF

BOGTJ15TR

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BH472349
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BOHNJ79TR BOHN Brassica oleracea genomic clone BOHNJ79, DNA
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Brassica oleracea.
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Eukaryorta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spérmatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spérmatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spérmatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spérmatophyta; Brassicalea; Brassica.
I (bases 1 to 775)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Opholished (2001)
Cohec. GSSs: BOHN/99TF
Contact: Chris Town
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/clone_lbb=BOHNS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
1 161 c 247 g 164 t
                                                                                                                                                                                                                                                                                                                                                                                 4 CTCGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGG 63
                                                                                                                                                                                                                                                                                                          0; Gaps
/organism="Brassica oleracea"
/strain="TO1000DH3"
/dbxref="taxon:3712"
/clone="BOHL572"
/clone=lib="BOHL"
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
/note: PHOS2; Site_1: BstXI; 2-3 kb sheared
/note: PHOS2; Site_1: BstXI; 2-3 kb sheared
/note: PHOS2; Site_1: BstXI; 2-3 kb sheared
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Best Local Similarity 87.8%; Score 72.4; DB 17; Length 775;
Best Local Similarity 87.8%; Pred. No. 2.5e-12;
Matches 79; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7912 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Fax: 301-838-0208 Fax: 301-838-0208 Fax: 501-808-0208 Fax: 502-809 Fax: TR Class: sheared ends...
                                                                                                                                                                                                                                                       Length 787;
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Pred. No. 2.1e-12;
0; Mismatches 14;
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/strain="TO1000H3"
/db_xref="taxon:3712"
/clone="BOHNJ79"
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BH424823
BH424823.1 GI:17610551
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Best Local Similarity 85.3%;
Matches 81; Conservative 0
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BH424823
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BH709230 836 bp DNA linear GSS 20-FEB-2002 BOMN033TR BO_2_3_KB Brassica oleracea genomic clone BOMN033, DNA
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSS: BOWNO33TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH653765 841 bp DNA linear GSS 19-FEB-20
BOMNX13TF BO_2_3_KB Brassica oleracea genomic clone BOMNX13, DNA
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                                                                                     /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstX1; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstX1 linkers"
146 c 195 g 262 t
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                                                      3 GCTCGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.5%; Score 71.8; DB 17; Length 836; 68.0%; Pred. No. 3.9e-12; Live 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, 1
Tel: 301-838-3523
Fax: 301-838-0208
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1. 836
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMNO33"
  Mismatches
                                                                                                                                                               63 GGGCAGGGATGGCTATATTCTGGGAGGGA 93 | 11|1 | 1|1 | 1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 | 1|1 |
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Best Local Similarity 68.0
Matches 100; Conservative
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  Matches
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BH653765
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Brassica oleracea
Brassica, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaea; Brassica.
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/db_xref="taxon:3712"
/clone="BOGIY5"
/clone=lib="BOGI"
/note="vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
a 142 c 191 g 272 t
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/db_xref="taxon:3712"
/clone="BOMLN95"
/clone=lib="BOL23_xBB.
/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
162 c 246 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 838;
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                                                                    Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
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DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72.2; DB 17; Length
Pred. No. 2.9e-12;
0; Mismatches 13; Indels
                 9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-3523
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Tel: 301-838-3523
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
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                                                                                                                                                                                                             Location/Qualifiers
1. .838
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BH668002.1 GI:18727985
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86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Conservative
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Best Local Similarity
Matches 80; Conserv
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GSS 19-FEB-2002

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BH474481
BOHHY09TR BOHH Brassica oleracea genomic clone BOHHY09, DNA
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Brassica oleracea.
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots;
Trosidae; eurosids II; Brassicalea; Brassica.
I (Bases I to 805)
Other GSSs; BOHHYOFF
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9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 805 / Acrani="Tol000bH3"
// Atrain="Tol000bH3"
// Clone="BondH"

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: Sheared ends.
Location/Qualifiers
1. 724
Actain="Parasica oleracea"
/strain="Tol000Bi3"
/clone="Bocaky5"
/clone="Boca
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BH474481
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Brassica oleracea.
Brassica oleracea.
Brassica oleracea. Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Sosidae; eurosidas II; Brassicales; Brassicaceae; Brassica.
Rosidae; eurosidas II; Brassicales; Brassicacea; Brassica.
Town.C.D., Van Aken,S., Utterback,T., and Fraser,C.M.
Town.C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Unpublished (2001)
Other_GSSS:.io.massica.
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases atrosids II) Brassicales; Brassica.
Town,C.D. Van Aken,S. Utterback,T. and Fraser,C.M.
Whole genome shockun sequencing of Brassica oleracea
Unpublished (2001)
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pred. No. 3.9e-12;
0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

    . 841
    /organism="Brassica oleracea"
/strain="TO1000DH3"

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BH418480.1 GI:17604208
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68.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 68.0
Matches 100; Conservative
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/strain="Landsberg erecta"
//dxxref="taxon:3702"
//clone="LERG142"
//clone="LERG142"
//clone=lib="LERG"
//clone=lib="LERG"
//note="Organ: Leaf; Vector: pucl9JK; Total genomic DNA was sheared to 0.40.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BHS37952 14-DEC-2001
BOGFU38TR BOGF Brassica oleracea genomic clone BOGFU38, DNA
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Brassica oleracea
Brassica, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                    polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
1713 Medical Center Dr., Rockville, MD 20850, USA
1714: 301 838 0200
Fax: 301 838 0208
Email: atétigr.org
For additional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thaliana chloroplast sequence (GB:AP000423)
Seq primer: TR
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 CTTGCTCCCTCGTGATCGATAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGG 102
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Fax: 301-838-0208
Enal: cdtown@tigr.org
Dnal: cdtown@tigr.org
Seq primer: TR
Class: sheared ends.
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Pred. No. 5e-12;
0; Mismatches 12;
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/organism="Arabidopsis thaliana"
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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86.7%;
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Best Local Similarity 86.73
Matches 78; Conservative
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BH537952
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         AUTHORS
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LERGI42TR LERG Arabidopsis thaliana genomic clone LERG142, DNA
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Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosidas II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Brassica.
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/db_xref-"taxon:3712"
/clone="BowFR11"
/clone="lbb-"BO_2_3_KB"
/clone=lib-"BO_2_3_KB"
/note="Vector: pHOS! site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS! site_1 blost b
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Ourpublished (2001)
Other_GSSs: BOMFRIITF
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39.0%; Score 71; DB 17; Length 84
Best Local Similarity 84.2%; Pred. No. 7.1e-12;
Matches 80; Conservative 0; Mismatches 15; Indels
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                                                          GGGCAGGGATGGCTATATTTCTGGGAGGGAGACCA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea.
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AQ962940/c
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DEFINITION
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BH721450
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BH646726 305 bp DNA linear GSS 19-FEB-2002
BOGWR48TF.1 BO_2_3_KB Brassica oleracea genomic clone BOGWR48, DNA
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Brassica oleracea.

Brassica oleracea.

Brassica oleracea.

Brassica oleracea.

Brassica oleracea.

Spermatophyta: Wagnoliophyta: endicotyledons: core endicots:

Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 305)

Whole genome shorgun sequencing of Brassica oleracea

Whole genome shorgun sequencing of Brassica oleracea

Other_GSSs: BOGWR48TF BOGWR48TR.1 BOGWR48TR
BH474703
BOGQ149TF BOGQ Brassica oleracea genomic clone BOGQ149, DNA
                                                                                                                                        GSS.
Brassica oleracea.
Brassica oleracea.
Brassica oleracea
Brassica oleracea: Unidiplantae; Streptophyta; eudicotyledons; core eudicots;
Bosidae; Unidiplantae; Brassicales; Brassica.
Brassica oleracea: Brassica oleracea
Town, C.D., van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BoGQ19TR
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/organia="Brassica oleracea"
/organia="Tol000bH3"
/db.xref="taxon:3712"
/clone="11b="BoGG149"
/clone="11b="BoGG0"
/clone="Yeachor: pHoS1; Site_1: BstXI; 2-3 kb sheared
/cote="Yeachor: pHoS1; Site_1: BstXI; 2-3 kb sheared
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/cote="Yeachor: phoS1; Site_1: BstXI linkers"
/cote: phoS1; Site_1: phoS1; Site_1: BstXI linkers"
/cote: phoS2; Site_1: phoS2; S
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38.98; Score 70.8; DB 17; Length 292;
Best Local Similarity 86.78; Pred. No. 5.9e-12;
Matches 78; Conservative 0; Mismatches 12; Indels 0
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Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                    152 GGGTAGGGTAGCTATATTTCTGGGAGCGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GGGCAGGGATGGCTATATTTCTGGGAGGGA 93
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BH646726
BH646726.1 GI:18704138
                                                                                                           BH474703.1 GI:17682814
                                                               sequence.
BH474703
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BH646726/c
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TITLE
JOURNAL
COMMENT
                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosida II; Brassicales; Brassicaea; Brassica.

1 (bases 1 to 238)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Onholished (2001)

Contact: Chris Town
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/clone_11b="BOGF"
/note="vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA. 17e1: 301-838-3523
Fax: 301-838-0208
Email: cdtownefilgr.org
DanA is from a doubled haploid provided by Tom Osborn. Seq primer: TR
Class: Sheared ends.
1. 0.238
                                                                                                                                                                                                  Length 199;
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